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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 75.9095 Seconds

(without alignments)
1349.183 Million cell updates/sec

Title: US-09-939-537-31_COPY_1_200

Perfect score: 1029

Sequence: 1 NMRGVPFRHLVLVQLALP.....TWTCVTLQNKVYFRIDIV 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	99.4	458	1	CD4_HUMAN
2	999	97.1	458	1	CD4_PANTR
3	912	88.6	458	1	CD4_MACP
4	910	88.4	458	1	CD4_MACP
5	904	87.9	458	1	CD4_MACP
6	903	87.8	458	1	CD4_MACP
7	885	86.0	458	1	CD4_CERAB
8	784	76.2	397	1	CD4_CERAB
9	783	76.1	397	1	CD4_CERAB
10	767	74.5	397	2	009261
11	767	74.5	397	2	009262
12	767	74.5	397	2	009263
13	767	74.5	397	2	009264
14	763	74.1	397	2	009265
15	763	74.1	397	2	009266
16	741.5	72.1	457	2	08H2T8
17	740.5	72.0	457	2	08H2T7
18	737.5	71.7	457	1	CD4_SAIISC
19	598	58.1	453	1	CD4_CANPA
20	597	58.0	455	2	0710E2
21	592	57.5	455	2	09X8T8
22	587.5	57.1	459	1	CD4_RABIT
23	562	54.6	432	2	06LBR1
24	557.5	54.2	474	2	P79355
25	553	53.7	457	2	06GYR3
26	531	51.6	406	2	06R3N3
27	531	51.6	447	2	06R3N4
28	488.5	47.5	457	1	CD4_RAT
29	475	46.2	457	1	CD4_MOUSE
30	467	45.4	457	2	061396
31	436.5	42.4	433	2	055054

ALIGNMENTS

RESULT 1	CD4_HUMAN	STANDARD;	PRT;	458 AA.
AC	P01730;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen			
DE	T4/Leu-3).			
GN	Name=CD4;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85254948; PubMed=2990730;			
RA	Maddon P.J., Littman D.R., Godfrey M., Maddon D.E., Chess L., Axel R.;			
RT	"The isolation and nucleotide sequence of a cDNA encoding the T cell			
RT	surface protein T4: a new member of the immunoglobulin gene family."			
RL	Cell 42:93-104(1985).			
RN	[2]			
RP	REVISION TO 26.			
RX	MEDLINE=89028665; PubMed=3263213; DOI=10.1016/0092-8674(88)90211-5;			
RA	Littman D.R., Maddon P.J., Axel R.;			
RT	"Corrected CD4 sequence."			
RL	Cell 55:541-541(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96303695; PubMed=8723724;			
RA	Anastasi-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,			
RT	"A gene-rich cluster between the CD4 and triosephosphate isomerase			
RT	genes at human chromosome 12p13."			
RL	Genome Res. 6:314-326(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A. AND VARIANT TRP-265.			
RX	MEDLINE=91216786; PubMed=1708753; DOI=10.1016/0198-8859(91)90077-M;			
RA	Hodge T.W., Sasse D.R., McDougal J.S.;			
RT	"Humans with OKT4-epitope deficiency have a single nucleotide base			
RT	change in the CD4 gene, resulting in substitution of TRP240 for			
RT	ARG240."			
RL	Hum. Immunol. 30:99-104(1991).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Krausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,			
RA	Krausberg R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsien F.,			
RA	Dhakshamo L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Urdin T.B., Tohiyuki S., Carninci P., Prange C.,			

32	400	38.9	86	2	077596	077596 mandrillus
33	400	38.9	86	2	077597	077597 mandrillus
34	397	38.6	86	2	077594	077594 cercopithec
35	397	38.6	86	2	077599	077599 theopithec
36	395	38.4	86	2	077595	077595 cercocobus
37	395	38.4	86	2	077595	077595 cercocobus
38	392	38.1	86	2	077598	077598 papio sp. (
39	388	37.7	86	2	077601	077601 lophocobus
40	380	37.2	86	2	077600	077600 lophocobus
41	380	36.9	78	2	06LCP8	06LCP8 homo sapien
42	357	34.7	71	2	013969	013969 homo sapien
43	305.5	29.7	99	2	029027	029027 sus scrofa
44	280.5	27.3	99	2	029028	029028 sus scrofa
45	172	16.7	482	2	090WB5	090WB5 anas platyr

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villallon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RT [6]
 RN SEQUENCE OF 28-424 FROM N.A.
 RP TISSUE=Blood;
 RC MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.,
 RT "Cloning and sequences of primate CD4 molecules: diversity of the
 RT cellular receptor for simian immunodeficiency virus/human
 RT immunodeficiency virus.";
 RT Eur. J. Immunol. 22:2973-2981(1992).
 RN [7]
 RN SEQUENCE OF 26-394, AND DISULFIDE BOND.
 RP MEDLINE=90078232; PubMed=2592374;
 RA Carr S.A., Hemling M.E., Polena-Waserman G., Sweet R.W., Anumula K.,
 RA Barr J.R., Huddleston M.J., Taylor P.,
 RT "Protein and carbohydrate structural analysis of a recombinant soluble
 RT CD4 receptor by mass spectrometry.";
 RT J. Biol. Chem. 264:21286-21295(1989).
 RN [8]
 RN SEQUENCE OF 26-40.
 RP PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RT Protein Sci. 13:2819-2824(2004).
 RN [9]
 RN REMOVAL FROM CELL SURFACE BY HIV-1 NFP, AND MUTAGENESIS OF MET-432;
 RP SER-433; 438-LEU-LEU-439 AND SER-440.
 RA "Nef induces CD4 endocytosis: requirement for a critical dileucine
 RT motif in the membrane-proximal CD4 cytoplasmic domain.";
 RT Cell 76:853-864(1994).
 RN [10]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 26-208.
 RP MEDLINE=91061801; PubMed=1701030; DOI=10.1038/348411a0;
 RA Wang J., Yan Y., Garrett T.P., Liu J., Rodgers D.W., Garlick R.L.,
 RA Tarr G.E., Husain Y., Reinherz E.L., Harrison S.C.,
 RT "Atomic structure of a fragment of human CD4 containing two
 RT immunoglobulin-like domains.";
 RT Nature 348:411-416(1990).
 RN [11]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-208.
 RP MEDLINE=91061882; PubMed=22471146; DOI=10.1038/348419a0;
 RA Rya S.-E., Kwong P.D., Truneh A., Porter T.G., Arthos J.,
 RA Rosenberg M., Dai X., Xiong N.-H., Axel R., Sweet R.W.,
 RA Hendrickson W.A.,
 RT "Crystal structure of an HIV-binding recombinant fragment of human
 RT CD4.";
 RT Nature 348:419-426(1990).
 RN [12]
 RN X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS) OF 26-388.
 RP MEDLINE=97311402; PubMed=9168119;
 RA Hu H., Kwong P.D., Hendrickson W.A.,
 RT "Dimeric association and segmental variability in the structure of
 RT human CD4.";
 RT Nature 387:527-530(1997).
 RN [13]
 RN PALMITOYLATION.
 RP MEDLINE=92317088; PubMed=1618861;
 RA Cripe B., Rose J.K.,

RT "Identification of palmitoylation sites on CD4, the human
 RT immunodeficiency virus receptor.";
 RT J. Biol. Chem. 267:13593-13597(1992).
 RN -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Removed from plasma
 CC membrane by HIV-1 Nef protein that increases clathrin-dependent
 CC endocytosis of this antigen to target it to lysosomal degradation.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD4 entry;
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd4.htm".
 CC -----
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 CC -----
 CC EMBL; M12807; AAA3572.1; -;
 CC EMBL; U47924; AA851309.1; -;
 CC EMBL; M35160; AAA16069.1; -;
 CC EMBL; BC025782; AA825782.1; -;
 CC PIR; A90872; RMHT4.
 CC PDB; 1CDH; X-ray; @=26-203.
 CC PDB; 1CDI; X-ray; @=25-203.
 CC PDB; 1CDJ; X-ray; @=26-203.
 CC PDB; 1CDU; X-ray; @=26-203.
 CC PDB; 1CDV; X-ray; @=26-203.
 CC PDB; 1GDM; X-ray; @=26-210.
 CC PDB; 1G9M; X-ray; @=26-210.
 CC PDB; 1GCT; X-ray; @=26-210.
 CC PDB; 1UT4; X-ray; @=26-203.
 CC PDB; 1Q68; NMR; A=421-458.
 CC PDB; 1WBR; NMR; A=427-445.
 CC PDB; 1WTO; X-ray; A/B=26-388.
 CC PDB; 1WIP; X-ray; A/B=26-388.
 CC PDB; 1WIO; X-ray; A/B=26-388.
 CC PDB; 3CD4; X-ray; @=26-207.
 CC GlycoSuiteDB; P01730; -;
 CC Genew; HGNC:1678; CD4.
 CC H-InvDB; HIX0023001; -;
 CC MIM; 186940; -;
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0042101; C:T-cell receptor complex; NAS.
 CC GO; GO:0015026; F:coreceptor activity; NAS.
 CC GO; GO:0015029; F:internalization receptor activity; TAS.
 CC GO; GO:0042289; F:MHC class II protein binding; NAS.
 CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
 CC GO; GO:0006955; P:immune response; NAS.
 CC GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; NAS.
 CC GO; GO:0030217; P:T-cell differentiation; NAS.
 CC GO; GO:0045058; P:T-cell selection; NAS.
 CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NAS.
 CC InterPro; IPR008424; CD2.
 CC InterPro; IPR000973; CD4_TCAg.
 CC InterPro; IPR007110; IG_Like.
 CC InterPro; IPR003596; IG_v.
 CC Pfam; PF00047; Ig_2.
 CC PRINTS; PR00692; CD4CANTIGEN.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS50835; IG_LIKE; 1.
 CC 3D-structure; Direct protein sequencing; Glycoprotein;
 CC Immune response; Immunoglobulin domain; Lipoprotein; Palmitate;
 CC Polymorphism; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458 T-cell surface glycoprotein CD4.
 FT DOMAIN 26 396 Extracellular (Potential).
 FT TRANSMEM 397 418 Potential.
 FT DOMAIN 419 458 Cytoplasmic (Potential).
 FT

```

FT  DOMAIN      26      125      Ig-like V-type.
FT  DOMAIN      126      203      Ig-like C2-type 1.

Query Match      99.4%; Score 1023; DB 1; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-77;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  MNRGVPFRHLVLTQALPAATQGNKVVYLGKGGDVEVLTCTASQKKSIOFHKNSNQIK 60
DB  1  MNRGVPFRHLVLTQALPAATQGNKVVYLGKGGDVEVLTCTASQKKSIOFHKNSNQIK 60
QY  61  IIGNGSSFLTGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVQL 120
DB  61  IIGNGSSFLTGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVQL 120
QY  121  LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPRGKNIQGGKTLVSQLELDQSG 180
DB  121  LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPRGKNIQGGKTLVSQLELDQSG 180
QY  181  TWTCVTLQNGKVEFKIDIV 200
DB  181  TWTCVTLQNGKVEFKIDIV 200

RESULT 2
CD4_PANTR      STANDARD;      PRT;      458 AA.
ID  CD4_PANTR
AC  P16704;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE  T4/Leu-3).
OS  Name=CD4;
OS  Pan troglodytes (Chimpanzee).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
OX  NCBI_TaxID=9598;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;
RA  Camerini D., Seed B.;
RT  "A CD4 domain important for HIV-mediated syncytium formation lies
RT  outside the virus binding site.";
RT  Cell 60:747-754(1990).
RN  [2]
RP  SEQUENCE OF 26-424 FROM N.A.
RC  TISSUE=Blood;
RX  MEDLINE=93049640; PubMed=1425921;
RA  Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT  "Cloning and sequences of simian immunodeficiency virus/human
RT  cellular receptor for simian immunodeficiency virus/human
RT  immunodeficiency virus.";
RT  Eur. J. Immunol. 22:2973-2981(1992).
CC  -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC  receptor interaction. May regulate T-cell activation.
CC  -1- SUBUNIT: Associates with p56-lck (By similarity).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC  -----
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CC  -----
DR  EMBL; M31135; AAA35407.1; -
DR  EMBL; X73323; CAAS1749.1; -
DR  PIR; B32722; RWCZ74.
DR  HSSP; P01730; IMIQ.

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DR  GO; GO:0042101; C:T-cell receptor complex, ISS.
DR  GO; GO:0015026; P:coreceptor activity, ISS.
DR  GO; GO:0042289; P:MHC class II protein binding, ISS.
DR  GO; GO:0006955; P:immune response, ISS.
DR  GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR  GO; GO:0030217; P:T-cell differentiation, ISS.
DR  GO; GO:0045058; P:T-cell selection, ISS.
DR  GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR  InterPro: IPR008424; CD2.
DR  InterPro: IPR000973; CD4_TcAg.
DR  InterPro: IPR007110; Ig_Like.
DR  InterPro: IPR003596; Ig_V.
DR  Pfam: PF00047; Ig_2.
DR  PRINTS; PR00692; CD4CANTIGEN.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Glycoprotein, Immune response, T-cell, Transmembrane.
KW  Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT  SIGNAL      1      25
FT  CHAIN      26      458
FT  DOMAIN      26      396
FT  TRANSMEM      397      418
FT  DOMAIN      419      458
FT  DOMAIN      26      125
FT  DOMAIN      126      203
FT  DOMAIN      204      317
FT  DOMAIN      318      374
FT  CARBOHYD      296      296
FT  CARBOHYD      325      325
FT  DISULFID      41      109
FT  DISULFID      155      184
FT  DISULFID      328      370
FT  LIPID      419      419
FT  LIPID      422      422
FT  CONFLICT      42      42
FT  CONFLICT      62      62
FT  CONFLICT      191      191
SQ  SEQUENCE      458 AA; 51057 MW; A7C3AC8A5257D3AD CRC64;

Query Match      97.1%; Score 999; DB 1; Length 458;
Best Local Similarity 97.5%; Pred. No. 3.6e-75;
Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1  MNRGVPFRHLVLTQALPAATQGNKVVYLGKGGDVEVLTCTASQKKSIOFHKNSNQIK 60
DB  1  MNRGVPFRHLVLTQALPAATQGNKVVYLGKGGDVEVLTCTASQKKSIOFHKNSNQIK 60
QY  61  IIGNGSSFLTGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVQL 120
DB  61  IIGNGSSFLTGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVQL 120
QY  121  LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPRGKNIQGGKTLVSQLELDQSG 180
DB  121  LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPRGKNIQGGKTLVSQLELDQSG 180
QY  181  TWTCVTLQNGKVEFKIDIV 200
DB  181  TWTCVTLQNGKVEFKIDIV 200

RESULT 3
CD4_MACFA      STANDARD;      PRT;      458 AA.
ID  CD4_MACFA
AC  P79185;
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE  T4/Leu-3).
OS  Name=CD4;
OS  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

```

OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9543;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymocyte;
 RA Tatum M., Yabe M., Yamada Y.K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC -----
 CC EMBL: D63349; BAA09672.1; -.
 CC HSSP: P01730; 1MBR.
 DR GO: GO:0042101; C: T-cell receptor complex; ISS.
 DR GO: GO:0015026; F: coreceptor activity; ISS.
 DR GO: GO:0042289; F: MHC class II protein binding; ISS.
 DR GO: GO:0006955; P: immune response; ISS.
 DR GO: GO:0045086; P: positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO: GO:0030217; P: T-cell differentiation; ISS.
 DR GO: GO:0045058; P: T-cell selection; ISS.
 DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro: IPR008424; CD2.
 DR InterPro: IPR000973; CD4_TcAg.
 DR InterPro: IPR007110; Ig_Like.
 DR Pfam: PR003596; Ig_V.
 DR Pfam: PR00047; Ig_2.
 DR PRINTS; PRO0692; CD4TCANTIGEN.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
 KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458
 FT DOMAIN 26 396
 FT TRANSMEM 397 418
 FT DOMAIN 419 458
 FT DOMAIN 26 125
 FT DOMAIN 126 203
 FT DOMAIN 204 317
 FT DOMAIN 318 374
 FT CARBOHYD 42 42
 FT CARBOHYD 296 296
 FT CARBOHYD 325 325
 FT DISULFID 41 109
 FT DISULFID 155 184
 FT DISULFID 328 370
 FT LIPID 419 419
 FT LIPID 422 422
 SQ SEQUENCE 458 AA; 50872 MW; 9105479FB5C56FF7 CRC64;
 Query Match 88.6%; Score 912; DB 1; Length 458;
 Beest Local Similarity 88.0%; Pred. No. 6.8e-68;
 Matches 176; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 121 LVFGITANSPTLHLQGGSLTTLTSPGSSPSVQCSPRGKNIQGGKTLVSQLELDDSG 180
 DB 121 LVFGITANSPTLHLQGGSLTTLTSPGSSPSVQCSPRGKNIQGGKTLVSQLELDDSG 180
 QY 181 TWCTCTVLQNKQKVEFKIDIV 200
 DB 181 TWCTCTVSQDQKTVFKIDIV 200
 RESULT 4
 ID CD4_MACFU STANDARD; PRT; 458 AA.
 AC P79184;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
 DE T4/Leu-3).
 GN Name=CD4;
 OS Macaca fuscata fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9543;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hashimoto O., Tatum M.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D63349; BAA09672.1; -.
 CC HSSP: P01730; 1MBR.
 DR GO: GO:0042101; C: T-cell receptor complex; ISS.
 DR GO: GO:0015026; F: coreceptor activity; ISS.
 DR GO: GO:0042289; F: MHC class II protein binding; ISS.
 DR GO: GO:0006955; P: immune response; ISS.
 DR GO: GO:0045086; P: positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO: GO:0030217; P: T-cell differentiation; ISS.
 DR GO: GO:0045058; P: T-cell selection; ISS.
 DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro: IPR008424; CD2.
 DR InterPro: IPR000973; CD4_TcAg.
 DR InterPro: IPR007110; Ig_Like.
 DR Pfam: PR003596; Ig_V.
 DR Pfam: PR00047; Ig_2.
 DR PRINTS; PRO0692; CD4TCANTIGEN.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
 KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458
 FT DOMAIN 26 396
 FT TRANSMEM 397 418
 FT DOMAIN 419 458
 FT DOMAIN 26 125
 FT DOMAIN 126 203
 FT DOMAIN 204 317
 FT DOMAIN 318 374
 FT CARBOHYD 42 42
 FT CARBOHYD 296 296
 FT CARBOHYD 325 325
 FT DISULFID 41 109
 FT DISULFID 155 184
 FT DISULFID 328 370
 FT LIPID 419 419
 FT LIPID 422 422
 SQ SEQUENCE 458 AA; 50872 MW; 9105479FB5C56FF7 CRC64;
 Query Match 88.6%; Score 912; DB 1; Length 458;
 Beest Local Similarity 88.0%; Pred. No. 6.8e-68;
 Matches 176; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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FT CARBOHYD 296 296 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 325 325 N-linked (GlcNAc... ) (By similarity).
FT DISULFID 41 109 By similarity.
FT DISULFID 155 184 By similarity.
FT DISULFID 328 370 By similarity.
FT LIPID 419 419 S-palmitoyl cysteine (By similarity).
FT LIPID 422 422 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 458 AA; 50828 MW; 76B3E7EF08185535 CRC64;

Query Match 88.4%; Score 910; DB 1; Length 458;
Best Local Similarity 87.5%; Pred. No. 1e-67;
Matches 175; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 NMRGVPFRLHLVLTQALLPAATQGNKVTLGKGDVVELTCTASOKKSIOFHKNNSNOIK 60
DB 1 NMRGIFPRLHLVLTQALLPAVTQGNKVTLGKGDVVELTCTASOKKSIOFHKNNSNOIK 60
QY 61 ILGNQSFLLTKGSPKLNDRADSRSLMDQGNFPLIKNLKIEDSDPYICEVEDQKEEVDI 120
DB 61 ILGIGSFLLTKGSPKLNDRADSRSLMDQGNFPLIKNLKIEDSDPYICEVEDQKEEVEL 120
QY 121 LVFGLTANSDFTHLLEQOSLTLTLESPGSSPSVQCRSPKRNIOGKRTLSVSOLEIADSG 180
DB 121 LVFGLTANSDFTHLLEQOSLTLTLESPGSSPSVQCRSPKRNIOGKRTLSVPLERQDSG 180
QY 181 TWTCTVLONOKVEPKIDIV 200
DB 181 TWTCTVSQDQKVEPKIDIV 200

RESULT 5
CD4_MACMU STANDARD; PRT; 458 AA.
ID CD4_MACMU STANDARD; PRT; 458 AA.
AC P16003; Q29617;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
GN Name=CD4;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBT_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;
RT "A CD4 domain important for HIV-mediated syncytium formation lies outside the virus binding site."
RL Cell 60:747-754(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Thymocytes;
RC "Molecular cloning and expression of macaque CD4s."
RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 28-424 FROM N.A.
RA TISSUE=Blood;
RC MEDLINE=93049640; PubMed=1425921;
RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus."
RL Eur. J. Immunol. 22:2973-2981(1992).
RN [4]
RP SEQUENCE OF 107-192 FROM N.A.
RA MEDLINE=98320644; PubMed=9656488;
RA Harris B.E., Disocell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini).";

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RL Mol. Biol. Evol. 15:892-900(1998).
CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC -1- receptor interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-lck (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC -----
DR EMBL; M31134; AAA6838.1; -
DR EMBL; D63347; BAA09671.1; -
DR EMBL; X73326; CAA51752.1; -
DR EMBL; AF057385; AAC25129.1; -
DR HSSP; P01730; 1MR.
DR GO; GO:0042101; C: T-cell receptor complex; ISS.
DR GO; GO:0015026; F: coreceptor activity; ISS.
DR GO; GO:0042289; F: MHC class II protein binding; ISS.
DR GO; GO:0065955; P: immune response; ISS.
DR GO; GO:0045086; P: positive regulation of interleukin-2 biosyn. .; ISS.
DR GO; GO:0030217; P: T-cell differentiation; ISS.
DR GO; GO:0045058; P: T-cell selection; ISS.
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4 TCAG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 458 T-cell surface glycoprotein CD4.
FT DOMAIN 26 396 Extracellular (Potential).
FT TRANSMEM 397 418 Potential.
FT DOMAIN 419 458 Cytoplasmic (Potential).
FT DOMAIN 26 125 Ig-like V-type.
FT DOMAIN 126 203 Ig-like C2-type 1.
FT DOMAIN 204 317 Ig-like C2-type 2.
FT CARBOHYD 318 374 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 325 325 N-linked (GlcNAc... ) (By similarity).
FT DISULFID 41 109 By similarity.
FT DISULFID 155 184 By similarity.
FT DISULFID 328 370 S-palmitoyl cysteine (By similarity).
FT LIPID 419 419 S-palmitoyl cysteine (By similarity).
FT LIPID 422 422 S-palmitoyl cysteine (By similarity).
FT CONFLICT 42 42 L -> S (in Ref. 1).
FT CONFLICT 62 62 L -> S (in Ref. 3).
FT CONFLICT 67 67 L -> S (in Ref. 2).
FT CONFLICT 169 169 K -> N (in Ref. 3).
FT CONFLICT 191 191 K -> P (in Ref. 2).
FT CONFLICT 248 248 R -> Q (in Ref. 2).
FT CONFLICT 265 265 R -> T (in Ref. 2).
FT CONFLICT 349 349 A -> T (in Ref. 2).
SQ SEQUENCE 458 AA; 50884 MW; 8BB80339F8EC08 CRC64;

Query Match 87.9%; Score 904; DB 1; Length 458;
Best Local Similarity 87.0%; Pred. No. 3.2e-67;
Matches 174; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 NMRGVPFRLHLVLTQALLPAATQGNKVTLGKGDVVELTCTASOKKSIOFHKNNSNOIK 60
DB 1 NMRGIFPRLHLVLTQALLPAVTQGNKVTLGKGDVVELTCTASOKKSIOFHKNNSNOIK 60

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QY 61 ILGNQSFLLTKGPKSLNDRADSRSLMDQGNFPLIKKLIKEDSTYICVEVDQKEEYOL 120
 DB 61 ILGIQGLPLTKGPKSLNDRADSRSLMDQGNFPLIKKLIKEDSTYICVEVDQKEEYOL 120
 QY 121 LVFGTLTANSDFHLLGQSLITLTLESPGSSPSVOCRRGNKIQGKTLVSQLELDQSG 180
 DB 121 LVFGTLTANSDFHLLGQSLITLTLESPGSSPSVOCRRGNKIQGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKQKVEFKIDIV 200
 DB 181 TWTCTVSQDKQKVEFKIDIV 200

RESULT 6
 CD4_MACNE STANDARD; PRT; 458 AA.
 AC 008340; P79196;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
 GN Name-CD4;
 OS Macaca nemestrina (Big-tailed macaque).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCB1_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hashimoto O., Tatsumi M.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 28-424 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus";
 RT Eur. J. Immunol. 22:2973-2981(1992).
 RL [1]
 CC -1 FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
 CC -1 SUBUNIT: Associates with p56-Lck (By similarity).
 CC -1 SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1 SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1 SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC EMBL; D63346; BAA09670.1; -;
 CC EMBL; X73325; CAA51751.1; -;
 DR HSP; P01730; IWBK.
 DR GO; GO:0042101; C:T-cell receptor complex; ISS.
 DR GO; GO:0015026; F:coreceptor activity; ISS.
 DR GO; GO:0042289; F:MHC class II protein binding; ISS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO; GO:0030217; P:T-cell differentiation; ISS.
 DR GO; GO:0045058; P:T-cell selection; ISS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro; IPR008424; CD2.
 DR InterPro; IPR000973; CD4_TcAg.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_2.
 DR PRINTS; PR00692; CD4TCANTIGEN.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
 KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458
 FT DOMAIN 26 396
 FT TRANSMEM 397 418
 FT DOMAIN 419 458
 FT DOMAIN 26 125
 FT DOMAIN 126 203
 FT DOMAIN 204 317
 FT DOMAIN 318 374
 FT DOMAIN 42 42
 FT CARBOHYD 296 296
 FT CARBOHYD 325 325
 FT DISULFID 41 109
 FT DISULFID 155 184
 FT DISULFID 328 370
 FT LIPID 419 419
 FT LIPID 422 422
 FT CONFLICT 57 57
 FT CONFLICT 91 91
 FT CONFLICT 105 105
 FT CONFLICT 113 113
 FT CONFLICT 302 302
 FT CONFLICT 349 349
 SQ SEQUENCE 458 AA; 50905 MW; 751A9BA2C8B3EE16 CRC64;

Query Match 87.8%; Score 903; DB 1; Length 458;
 Best Local Similarity 87.0%; Pred. No. 3.8e-67;
 Matches 174; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNRGVPFRLHLVLTQALLPATQGNKVVLGKGDVLELTCTASQKKSIGPHMKNNOIK 60
 DB 1 MNRGVPFRLHLVLTQALLPATQGNKVVLGKGDVLELTCTASQKKSIGPHMKNNOIK 60
 QY 61 ILGNQSFLLTKGPKSLNDRADSRSLMDQGNFPLIKKLIKEDSTYICVEVDQKEEYOL 120
 DB 61 ILGIQGLPLTKGPKSLNDRADSRSLMDQGNFPLIKKLIKEDSTYICVEVDQKEEYOL 120
 QY 121 LVFGTLTANSDFHLLGQSLITLTLESPGSSPSVOCRRGNKIQGKTLVSQLELDQSG 180
 DB 121 LVFGTLTANSDFHLLGQSLITLTLESPGSSPSVOCRRGNKIQGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKQKVEFKIDIV 200
 DB 181 TWTCTVSQDKQKVEFKIDIV 200

RESULT 7
 CD4_CERAE STANDARD; PRT; 458 AA.
 ID -CD4 CERAE
 AC 008338; 002805; 077593; 028217;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
 GN Name-CD4;
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 NC NCB1_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hashimoto O., Tatsumi M.;
 RL "Molecular cloning and expression of african green monkey CD4.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 28-424 FROM N.A.
 RC TISSUE=Blood;

RX MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the
 RT cellular receptor for simian immunodeficiency virus/human
 RT immunodeficiency virus.";
 RL Eur. J. Immunol. 22:2973-2981 (1992).
 RN (3)
 RP SEQUENCE OF 28-424 FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=98017879; PubMed=9379478;
 RA Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Machiet C.,
 RA Corbet S., Barre-Sinoussi F., Allan J.S.;
 RT "Relation between phylogeny of African green monkey CD4 genes and
 RT their respective simian immunodeficiency virus genes.";
 RL J. Med. Primatol. 26:120-126 (1997).
 RN [4]
 RP SEQUENCE OF 107-192 FROM N.A.
 RX MEDLINE=98320644; PubMed=9656488;
 RA Harris B.E., Diocelli T.R.;
 RT "Nucleic acid sequences and the phylogenetic relationships of the
 RT mangabey (Primates: Papionini)";
 RL Mol. Biol. Evol. 15:892-900 (1998).
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC -----
 DR EMBL; DB6589; BAA13132.1; -;
 DR EMBL; X73332; CA51748.1; -;
 DR EMBL; AF001226; AAB60873.1; -;
 DR EMBL; AF001228; AAB60875.1; -;
 DR EMBL; AF057380; AAC25124.1; -;
 DR HSSP; P01730; 1MIO.
 DR GO; GO:0042101; C-T-cell receptor complex; ISS.
 DR GO; GO:0015026; F:coreceptor activity; ISS.
 DR GO; GO:0042289; F:MHC class II protein binding; ISS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO; GO:0030217; P:T-cell differentiation; ISS.
 DR GO; GO:0045058; P:T-cell selection; ISS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro; IPR008424; CD2.
 DR InterPro; IPR000973; CD4_TCRG.
 DR InterPro; IPR007110; Ig-1Ike.
 DR Pfam; PF00047; Ig_2.
 DR PRINTS; PR00692; CD4TCANTIGEN.
 DR PROSITE; PS00835; IG_LIKE_1.
 DR GlycoProtein; Immune response; Immunoglobulin domain; Lipoprotein;
 DR Palmitate; Repeat; Signal; T-cell; Transmembrane.
 KW SIGNL.
 FT CHAIN 1 25
 FT DOMAIN 26 458
 FT TRANSMEM 397 418
 FT DOMAIN 419 458
 FT DOMAIN 26 125
 FT DOMAIN 126 203
 FT DOMAIN 204 317
 FT DOMAIN 318 374
 FT CARBOHYD 42 42
 FT CARBOHYD 281 281
 FT CARBOHYD 296 296
 FT CARBOHYD 325 325
 FT DISULFID 41 109
 By similarity.
 T-cell surface glycoprotein CD4.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 Ig-1-like V-type.
 Ig-1-like C2-type 1.
 Ig-1-like C2-type 2.
 Ig-1-like C2-type 3.
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 By similarity.

FT DISULFID 155 184 By similarity.
 FT DISULFID 328 370 By similarity.
 FT LIPID 419 419 S-palmitoyl cysteine (By similarity).
 FT LIPID 422 422 S-palmitoyl cysteine (By similarity).
 FT CONFLICT 46 46 K -> N (in Ref. 2 and 3; AAB60875).
 FT CONFLICT 59 59 K -> T (in Ref. 3; AAB60873).
 FT CONFLICT 115 115 G -> E (in Ref. 1).
 FT CONFLICT 165 165 G -> V (in Ref. 3; AAB60873 and 4).
 FT CONFLICT 200 200 M -> V (in Ref. 2 and 3).
 FT CONFLICT 227 227 F -> L (in Ref. 3; AAB60873).
 FT CONFLICT 271 271 K -> E (in Ref. 3; AAB60873).
 FT CONFLICT 281 281 N -> H (in Ref. 3; AAB60873).
 SQ SEQUENCE 458 AA; 51158 MW; FC523D2EDDIF72E7 CRC64;
 Query Match 86.0%; Score 885; DB 1; Length 458;
 Best Local Similarity 85.5%; Pred. No. 1,2e-65;
 Matches 171; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MNRGVPFRHLVLTQALPAATQGNKVVYLGKGDVETCTASQKKSIOFHKNSNQIK 60
 DB 1 MMNGIFPRHLVLTQALPAATQGNKVVYLGKGDVETCTASQKKSIOFHKNSNQIK 60
 QY 61 ILGNQSPFLTKGSPKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEEVL 120
 DB 61 ILGNQSPFLTKGSPKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEEVL 120
 QY 121 LVFGLTANSDTHLLQGSLLTLTLESPGSSPSVQCSPPGKNIQGKKTLSVSGLEQDSG 180
 DB 121 LVFGLTANSDTHLLQGSLLTLTLESPGSSPSVQCSPPGKNIQGKKTLSVSGLEQDSG 180
 QY 181 TWTCVLTQNKQKVFPIKIDV 200
 DB 181 TWTCVLTQNKQKVFPIKIDV 200
 QY 181 TWTCVLTQNKQKVFPIKIDV 200
 DB 181 TWTCVLTQNKQKVFPIKIDV 200
 RESULT 8
 CD4_CERTO
 ID CD4_CERTO STANDARD; PRT; 397 AA.
 AC 008536;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
 DE (Fragment).
 GN Name=CD4;
 OS Cercopithecus torquatus alyx (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_Taxid=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the
 RT cellular receptor for simian immunodeficiency virus/human
 RT immunodeficiency virus.";
 RL Eur. J. Immunol. 22:2973-2981 (1992).
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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Query Match	Similarity	76.2% Score 784; DB 1; Length 397;
Best Local	Similarity 87.3%; Pred. No. 2,9e-57;	
Matches 151; Conservative 11; Mismatches 11; Indels 0; Gaps 0.		
Db	1 VLAKGKDPYVELTCTASQKTSIQFHWKNSNQITILNOCGSEFLTKGSKINDRADSRSLW 87	
Qy	88 DOGNPRLIKKILKIEDSPDYCEVEDPKKEVQLVFLGLTANSDTHLLQGSLTTLTLESP 147	
Db	61 DQGCTSMIIKKIKIEDSTFYCEVENKKEVELLVFLGLTANSDTHLLQGSLTTLTLESP 120	
Qy	148 GSSPSVQCRSPRGKNIQCGKTLVSQILFLDQSGTCTTVLONOKKVEFKIDV 200	
Db	121 GSPSVKCRSPRGKNIQCGRTLSVFLERQDSGTCTVSDQKTFEKKIDV 173	
RESULT 9		
CD4_ERYPA	STANDARD; PRT; 397 AA.	
AC	008339;	
DT	01-FEB-1995 (Rel. 31, Created)	
DT	01-FEB-1995 (Rel. 31, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)	
DE	(fragment).	

Query Match	Best Local Similarity	Score 783; DB 1; Length 397;
Matches 150; Conservative 10; Mismatches 13; Indels 0; Gaps 0;		
28	VVLGKGPVETLCTASQKSIQPHWNNSNQIKILNQGSFLTKGPSKLNDAADRSLM	87


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Db      1 VVLGKGGDTVELTCNSQKTTTFHWNKNSNQIKLGQSGFLTKGPKLNDRDRSRSLW 60
Qy      88 DQGNFPLIINKLIEBDSITYICEVEDQKEVOLLVFGLTANSPTHLQGGSLTLTLESPP 147
Db      61 DQCFSMIINKLIEBSEITYICEVENKKEVELLVFGLTANSPTHLQGGSLTLTLESPP 120
Qy      148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNOKVEFKIDIV 200
Db      121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNOKVEFKIDIV 173

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RESULT 10

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009261 PRELIMINARY; PRT; 397 AA.
AC 009261;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD4 (Fragment).
GN Name=CD4;
OS Cercopithecus sabaenus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001225; AAB60872.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-sect; 2.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT TER 397
SQ SEQUENCE 397 AA; 43945 MW; 80C963B92A868CD3 CRC64;

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Query Match 74.5%; Score 767; DB 2; Length 397;
 Best Local Similarity 85.5%; Pred. No. 7.6e-56;
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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Qy      28 VVLGKGGDTVELTCNSQKSIQFHWKNSNQIKLGQSGFLTKGPKLNDRDRSRSLW 87
Db      1 VVLGKGGDTVELTCNSQNTTTFHWNKNSNQIKLGQSGFLTKGSKLDRDRSRSLW 60
Qy      88 DQGNFPLIINKLIEBDSITYICEVEDQKEVOLLVFGLTANSPTHLQGGSLTLTLESPP 147
Db      61 DQCFSMIINKLIEBSEITYICEVENKKEVELLVFGLTANSPTHLQGGSLTLTLESPP 120
Qy      148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNOKVEFKIDIV 200
Db      121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNOKVEFKIDIV 173

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RESULT 11
 009262 PRELIMINARY; PRT; 397 AA.
 AC 009262;

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DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD4 (Fragment).
GN Name=CD4;
OS Cercopithecus tanzanus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001221; AAB60868.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-sect; 2.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT TER 397
SQ SEQUENCE 397 AA; 43954 MW; CF7F2F5D8233580D CRC64;

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Query Match 74.5%; Score 767; DB 2; Length 397;
 Best Local Similarity 85.5%; Pred. No. 7.6e-56;
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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Qy      28 VVLGKGGDTVELTCNSQKSIQFHWKNSNQIKLGQSGFLTKGPKLNDRDRSRSLW 87
Db      1 VVLGKGGDTVELTCNSQNTTTFHWNKNSNQIKLGQSGFLTKGSKLDRDRSRSLW 60
Qy      88 DQGNFPLIINKLIEBDSITYICEVEDQKEVOLLVFGLTANSPTHLQGGSLTLTLESPP 147
Db      61 DQCFSMIINKLIEBSEITYICEVENKKEVELLVFGLTANSPTHLQGGSLTLTLESPP 120
Qy      148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNOKVEFKIDIV 200
Db      121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNOKVEFKIDIV 173

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RESULT 12
 009263 PRELIMINARY; PRT; 397 AA.
 AC 009263;

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DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD4 (Fragment).
GN Name=CD4;
OS Cercopithecus tanzanus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and

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RT their respective simlan immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001222; AAB60868.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-set; 2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 397 AA; 43994 MW; A3CD031535A51524 CRC64;

Query Match 74.5%; Score 767; DB 2; Length 397;
Best Local Similarity 85.5%; Pred. No. 7.6e-56;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDTVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 87
DB 1 VVLGKKGDTVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 60

QY 88 DQGNPLIINKLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHTLLOQGSLLTLTLESP 147
DB 61 DQGFSPMIINKLKIEDSETTYICEVENKEEVELLVFGLTANSDPHTLLOQGSLLTLTLESP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWTCVTONQKVEFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWTCVTONQKVEFKIDIV 173

RESULT 13
Q95NE9 PRELIMINARY; PRT; 397 AA.
AC Q95NE9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C04 (Fragment).
GN Name=C04;
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RT Corbet S., Barre-Sinoussi F., Allan J.S.,
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simlan immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001227; AAB60874.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-set; 2.
DR Pfam; PF00047; IGV; 1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43946 MW; 21C3E30882ABFC0 CRC64;

Query Match 74.5%; Score 767; DB 2; Length 397;
Best Local Similarity 85.5%; Pred. No. 7.6e-56;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDTVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 87
DB 1 VVLGKKGDTVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 60

QY 88 DQGNPLIINKLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHTLLOQGSLLTLTLESP 147
DB 61 DQGFSPMIINKLKIEDSETTYICEVENKEEVELLVFGLTANSDPHTLLOQGSLLTLTLESP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWTCVTONQKVEFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWTCVTONQKVEFKIDIV 173

RESULT 14
O09259 PRELIMINARY; PRT; 397 AA.
AC O09259;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C04 (Fragment).
GN Name=C04;
OS Cercopithecus sabaueus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RT Corbet S., Barre-Sinoussi F., Allan J.S.,
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simlan immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001223; AAB60870.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-set; 2.
DR Pfam; PF00047; IGV; 1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 397 AA; 43881 MW; 7CB39AD0F8506C81 CRC64;

Query Match 74.1%; Score 763; DB 2; Length 397;
Best Local Similarity 85.0%; Pred. No. 1.7e-55;
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDTVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 87
DB 1 VVLGKKGDTVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 60

QY 88 DQGNPLIINKLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHTLLOQGSLLTLTLESP 147
DB 61 DQGFSPMIINKLKIEDSETTYICEVENKEEVELLVFGLTANSDPHTLLOQGSLLTLTLESP 120

QY 148 GSSPSPVQCRSPRKNIGQKTLISVSQLDSDSGTWCTVLQNKQKVEFKIDIV 200
DB 121 GSSPSPVYKCRSPRKNIGQKTLISVSQLDSDSGTWCTVNSQDQNTVEFKIDIV 173

RESULT 15

ID 009260 PRELIMINARY; PRT; 397 AA.
AC 009260;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD4 (fragment).
GN Name=CD4;
OS Cercopithecus sabaues.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euleleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
Corbet S., Barre-Sinoussi F., Allan J.S.,
RT "Relation between phylogeny of African green monkey CD4 genes and
their respective simian immunodeficiency virus genes."
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001224; AAB60871.1; -.
DR HSSP; P01730; IMIO.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-sec; 2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGY; 1.
DR PROSITE; PS50835; IGY_LIKE; 1.
FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43882 MW; 478BB277E992EBE89 CRC64;

Query Match 74.1%; Score 763; DB 2; Length 397;
Best Local Similarity 85.0%; Pred. No. 1.7e-55;
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKGGDTVELTCTASQKSIQFHMNSNQIKILGQGSFLTKGPKLMDRADSRRLW 87
DB 1 VVLGKGGDTVELTCTANSQKTTTQFHMNSNQIKILGQGSFLTKGSKLMDRIDSRKSLW 60
QY 88 DQGNFPLIIKNLKIIBSDTYICEVEDQKEVQLVFGLTANSPTHLQGSLLTLESPP 147
DB 61 DQCFPMIINKLKIIBSETYICEVENKEVEVLVFGLTANSPTHLQGSLLTLESPP 120
QY 148 GSSPSPVQCRSPRKNIGQKTLISVSQLDSDSGTWCTVLQNKQKVEFKIDIV 200
DB 121 GSSPSPVYKCRSPRKNIGQKTLISVSQLDSDSGTWCTVNSQDQNTVEFKIDIV 173

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